

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 92.2921 Seconds

(without alignments)  
1579.326 Million cell updates/sec

Title: US-09-698-781-17  
Perfect score: 44  
Sequence: 1 TLFPVLLFL 9

Scoring table:

BLOSUM62  
Xgapop 10.0, Ygapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ .p2n.model -DEV-xlh  
-Q/cgna\_1/USPto.spool/US09698781/rnat\_07032003.083459.5329/app.query.fasta\_1.654  
-DB-EST -QFMT-fastlap -SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST=45  
-DOCLALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT-pio -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09698781.gcgn\_1.1.2463-ernat\_07032003.083459.5329 -NCPU=6 -ICPU=3  
-NO\_XLPY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV-TIMEOUT=120  
-WARN-TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	547	9	AL703262
2	42	95.5	353	14	BQ666605
3	41	93.2	308	14	BM832007
4	41	93.2	407	14	BM822727
5	41	93.2	447	10	AM009767
6	41	93.2	461	10	BB839116
7	41	93.2	538	14	BM751298
8	41	93.2	575	10	BE036163
9	41	93.2	619	17	A2108486
10	41	93.2	693	9	AU138699
11	41	93.2	722	12	BG718279
12	41	93.2	724	10	BE545083
13	41	93.2	767	13	BM013479
14	41	93.2	785	14	BM715733
15	41	93.2	813	12	BG574770
16	41	93.2	861	14	BQ441085
17	41	93.2	869	17	A2539955
18	41	93.2	898	17	A2668486
19	41	93.2	921	17	BH132102
20	41	93.2	972	14	BQ068805
21	41	93.2	1018	14	BQ071051
22	41	93.2	1072	14	BQ052048
23	41	93.2	1075	14	BQ069622
24	41	93.2	1094	12	BG118306
25	41	93.2	1117	10	BE372269
26	41	93.2	1187	17	A2686289
27	40	90.9	349	13	B1178406
28	40	90.9	421	10	BE177732
29	40	90.9	469	17	AQ0209341
30	40	90.9	578	17	A2849527
31	40	90.9	643	14	BQ120863
32	40	90.9	656	14	BQ050928
33	40	90.9	655	10	BB344289
34	40	90.9	959	17	CNS0701T
35	39	88.6	103	9	A1956273
36	39	88.6	105	17	A2828001
37	39	88.6	186	9	A1572293
38	39	88.6	192	12	BF819364
39	39	88.6	270	17	TA383B01Q
40	39	88.6	297	17	B82165
41	39	88.6	309	12	BF331555
42	39	88.6	318	12	BF879720
43	39	88.6	334	9	AA883350
44	39	88.6	340	9	AA007134
45	39	88.6	342	10	BB870337

# ALIGNMENTS

RESULT 1	AL703262	547 bp	mRNA	linear	EST 22-MAR-2002
LOCUS	AL703262				
DEFINITION	DKFZp686K1819_r1 686 (synonym: hicc3) Homo sapiens CDNA clone				
ACCESSION	AL703262.1				
VERSION	AL703262.1				
KEYWORDS	GI:19686617				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.)				
TITLE	EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann				

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Poustka A.J.  
Department Lehnach  
Max-Planck-Institute for Molecular Genetics  
Inhestrasse 73, 14195 Berlin, Germany  
Tel: +49-30-84131623  
Fax: +49-30-84131128

Email: poustka@mpg-berlin-dahlem.mpg.de  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No 5' sequence available.  
This clone (DKFZp686K1819) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

source  
1..547  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp686K1819"  
/clone\_lib="686 (synonym: hicc3)"  
/tissue\_type="human skeletal muscle"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pTRIPLEX2; Site\_1: SfilA; Site\_2: SfilB;  
cDNA-collection"

BASE COUNT  
ORIGIN

170 a 120 c 120 g 137 t

## Alignment Scores:

Pred. No.: 373 Length: 547  
Score: 44.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-698-781-17 (1-9) x AL703262 (1-547)

OY 1 ThreupheProValleuPheleu 9  
|||||  
Db 46 ACATTATTCACAGCTGCTTCTCTG 72

## RESULT 2

BQ966605 353 bp mRNA linear EST 21-AUG-2002  
LOCUS BQ966605  
DEFINITION QHB27F16, yf, ab1 QH, ABCDI sunflower RHA801 Helianthus annuus cDNA  
clone QHB27F16, mRNA sequence.

ACCESSION BQ966605  
VERSION BQ966605.1 GI:22383710  
KEYWORDS EST.  
SOURCE common sunflower.  
ORGANISM Helianthus annuus

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; easterids II; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
1 (bases 1 to 353)

REFERENCE  
AUTHORS

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Davelle, D., Chevalier, P., Ziegler, J., Ellison,  
P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,  
Church, S., Jackson, L. and Bradford, K.  
lettuce and sunflower ESTs from the Compositae Genome Project  
http://compgenomics.ucdavis.edu/  
Unpublished (2002)

JOURNAL  
COMMENT

Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@atgc.org [michelmore@evemail.ucdavis.edu]  
Singleton, see http://cgpdb.ucdavis.edu/ for details.  
Plate: QHB27 row: F column: 16.  
Location/Qualifiers  
1..353

FEATURES  
source

/organism="Helianthus annuus"  
/cultivar="RHA801"  
/db\_xref="taxon:4232"  
/clone="QHB27F16"  
/clone\_lib="QH, ABCDI sunflower RHA801"  
/lab\_host="E.coli"  
/note="Vector: pBRCDNA5flab: The library was constructed  
from 11 different sources of RNA from a single genotype.  
separate cDNAs were generated using primers that  
incorporated unique 5' and 3' tags to distinguish each  
source of RNA. cDNAs were then pooled, size-fractionated,  
directionally cloned into a custom medium-copy vector and  
transformations made with four size classes to minimize  
size bias. Details of each source of RNA and library  
construction can be obtained at http://cgpdb.ucdavis.edu/  
TAG\_LIB-QH, ABCDI sunflower RHA801  
TAG\_TISSUE=roots  
TAG\_SEQ=GTTCACGCG"

BASE COUNT  
ORIGIN

104 a 58 c 95 g 96 t

## Alignment Scores:

Pred. No.: 494 Length: 353  
Score: 42.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 88.89% Mismatches: 0  
Query Match: 95.45% Indels: 0  
DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BQ966605 (1-353)

OY 1 ThreupheProValleuPheleu 9  
|||||  
Db 217 ACTATTTTCCCGCTCTTCTTCTT 191

## RESULT 3

BM832007 308 bp mRNA linear EST 06-MAR-2002  
LOCUS BM832007/c  
DEFINITION K-EST0106159 S20T665307 Homo sapiens cDNA clone S20T665307-32-C08  
5', mRNA sequence.

ACCESSION BM832007  
VERSION BM832007.1 GI:19188416  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 308)  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

REFERENCE  
AUTHORS

Kim, Y.S.  
ZIC Frontiers Korean EST Project 2001  
Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsungem@kribb.re.kr  
Plate: 32 row: C column: 08  
High quality sequence stop: 308.

## FEATURES

source  
1..308  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

```
/clone-"S20T665307-32-C08"
/clone.lib-"S20T665307"
/sex="M"
/lab_host-"Top10F"
/Note-"Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI. The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT      117 a      54 c      99 g      38 t
ORIGIN

Alignment Scores:
Pred. No.:      629      Length:      308
Score:          41.00     Matches:      8
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 88.89%  Mismatches:  0
Query Match:    93.18%     Indels:      0
DB:             14        Gaps:        0

US-09-698-781-17 (1-9) x BM832007 (1-308)

Qy      1  ThrleupheProvalleuLeupheleu 9
DB      133 ACTCTCTTCTCTCTCTCTTTTCTT 107

RESULT 4
BM822727/c      407 bp      mRNA      linear      EST 06-MAR-2002
LOCUS          BM822727      K-EST0092951 S20T665307 Homo sapiens CDNA clone S20T665307-17-H07
DEFINITION     5', mRNA sequence.
ACCESSION      BM822727.1 GI:19179140
VERSION        EST.
KEYWORDS       human.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 407)
AUTHORS        Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
                Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                Kim,Y.S.
JOURNAL        21C Frontier Korean EST Project 2001
COMMENT        Unpublished (2002)
                Contact: Kim YS
                Genome Research Center
                Korea Research Institute of Bioscience & Biotechnology
                52 Eoan-dong Yuseong-gu, Daejeon 305-333, South Korea
                Tel: +82-42-860-4470
                Fax: +82-42-860-4409
                Email: yongsung@mail.kribb.re.kr
                Plate: 17 row: H column: 07
                High quality sequence stop: 407.
                Location/Qualifiers
                1..407
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="S20T665307-17-H07"
                /clone.lib="S20T665307"
                /sex="M"
                /lab_host="Top10F"
                /Note-"Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
```

```
Site_2: NotI. The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT      132 a      85 c      129 g      61 t
ORIGIN

Alignment Scores:
Pred. No.:      889      Length:      407
Score:          41.00     Matches:      8
Percent Similarity: 100.00%  Conservative: 1
Best Local Similarity: 88.89%  Mismatches:  0
Query Match:    93.18%     Indels:      0
DB:             14        Gaps:        0

US-09-698-781-17 (1-9) x BM822727 (1-407)

Qy      1  ThrleupheProvalleuLeupheleu 9
DB      71 ACTCTTCTCTCTCTCTTTTCTT 45

RESULT 5
AM009767/c      447 bp      mRNA      linear      EST 10-SEP-1999
LOCUS          AM009767      W887B09.x1 NCI_CGAP_C03 Homo sapiens CDNA clone IMAGE:2504921 3',
DEFINITION     RNA sequence.
ACCESSION      AM009767      AM009767.1 GI:5858545
VERSION        AM009767
KEYWORDS       human.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 447)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
                Unpublished (1997)
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs@mail.nih.gov
                Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
                Ph.D.
                CDNA Library Preparation: M. Bento Soares, Ph.D.
                CDNA Library Arraying: Greg Lennon, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/ULNL at:
                www.bio.lnl.gov/btrp/image/image.html
                Seq primer: -40UP from Gibco.
                Location/Qualifiers
                1..447
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2504921"
                /clone.lib="NCI_CGAP_C03"
                /sex="pooled"
                /tissue_type="Colon"
                /lab_host="DH10B"
                /Note-"Vector: p77T3D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was prepared from 12 pooled bulk tumor samples and primed
                with a Not I - oligo(dt) primer. Double-stranded cDNA was
```

ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization.

BASE COUNT 171 a 67 c 139 t

## ALIGNMENT SCORES:

Pred. No.: 998 Length: 447  
Score: 41.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 88.89% Mismatches: 0  
Query Match: 93.18% Indels: 0  
DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x AM009767 (1-447)

Oy 1 Thrlaupheovalleupheleu 9

Db 332 ACCTGTTCTTCTTATTTCTCTG 306

## RESULT 6

LOCUS

BB839116 461 bp mRNA linear EST 21-NOV-2001

DEFINITION BB839116 RIKEN full-length enriched, 8 cells embryo Mus musculus

CDNA clone E860007012 5', mRNA sequence.

ACCESSION BB839116

VERSION BB839116.1 GI:17039847

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Euteleostomi:

AUTHORS 1 (bases 1 to 461)

Unpublished (2001)

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, K., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watabiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura

, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multichannel sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

## FEATURES

source

e mouse tissues.  
Location/Qualifiers

1..461

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="E860007012"

/clone\_lib="RIKEN full-length enriched, 8 cells embryo"

/cell\_type="8 cells"

/dev\_stage="8 cells embryo"

/note="Vector: pSPORI1, Site1: SalI, Site2: NotI. This

clone is among a rearranged set of 15,247 clones from 11

embryo cDNA libraries (including preimplantation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos

, and E12.5 female mesonephros/gonad) and one newborn

ovary cDNA library. Average insert size 1.5 kb. All

source libraries are cloned unidirectionally with Oligo(dT

)-Not primers. References include: (1) Genome-wide

expression profiling of mid-gestation placenta and embryo

using a 15,000 mouse developmental cDNA microarray, 2000,

Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132. (2)

Large-scale cDNA analysis reveals phased gene expression

patterns during preimplantation mouse development, 2000,

Development, 127: 1737-1749. (3) Genome-wide mapping of

unselected transcripts from extraembryonic tissue of

7.5-day mouse embryos reveals enrichment in the t-complex

and under-representation on the X chromosome, 1998, Hum

Mol. Genet. 7: 1967-1978."

BASE COUNT 158 a 74 c 83 g 146 t

## ORIGIN

## ALIGNMENT SCORES:

Pred. No.: 1.04e+03 Length: 461  
Score: 41.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 88.89% Mismatches: 0  
Query Match: 93.18% Indels: 0  
DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x BB839116 (1-461)

Oy 1 Thrlaupheovalleupheleu 9

Db 198 ACTCTTTTCCACGCTCTTCTCTC 172

## RESULT 7

LOCUS

BM751298/c

DEFINITION

BM751298

VERSION

BM751298.1

KEYWORDS

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsungemall.kribb.re.kr

Plate: 12 row: H column: 12

High quality sequence stop: 538.

FEATURES  
SOURCE

Location/Qualifiers  
1. 538  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="S9SNU601-12-H12"  
/clone\_lib="S9SNU601"  
/sex="M"  
/tissue\_type="Ascites"  
/cell\_type="Epithelial"  
/cell\_line="SNU-601"  
/lab\_host="Top10F"  
/note="Organ: Stomach; Vector: pME18-FL3; Site:1: XhoI;  
Site:2: XhoI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAR) and then deapped  
with tabacco acid pyrophosphatase (TAP). The deapped  
intact mRNA was ligated with DNA-RNA linker including SfiI  
site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized with Superscript II using SfiI  
oligo-dT primer. After first strand synthesis, RNA was  
degraded by NaOH treatment and cDNA was amplified by PCR  
reaction. The PCR products were digested with SfiI and  
cloned into DraIII- digested pME18-FL3 vector. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F' by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

BASE COUNT  
ORIGIN

196 a 104 c 102 g 136 t

## Alignment Scores:

Pred. No.: 1.26e+03 Length: 538  
Score: 41.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 86.89% Mismatches: 0  
Query Match: 93.18% Indels: 0  
DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BM751298 (1-538)

OY 1 ThrleupheProvalleupheleu 9  
|||||  
DB 48 ACCTGTTCCGCTCTCTTTCTG 22

RESULT 8  
BE036163

LOCUS BE036163 575 bp mRNA linear EST 07-JUN-2000  
DEFINITION MO20E02 MO Mesembryanthemum crystallinum cDNA 5', mRNA sequence.  
ACCESSION BE036163  
VERSION BE036163.1 GI:83311172  
KEYWORDS EST.

SOURCE  
ORGANISM

Common Iceplant.  
Mesembryanthemum crystallinum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllidae; Caryophyllales; Alzooaceae; Mesembryanthemum.  
1 (bases 1 to 575)

REFERENCE  
AUTHORS

Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,  
H., Kawasak, S., McCollough, A., Michalowski, C.B., Palacio, C.,  
Scara, G., Wheeler, M. and Zepeda, G.R.  
Functional Genomics of Plant Stress Tolerance  
Unpublished (2000)  
Contact: Michalowski, C.B.  
University of Arizona  
Bio Sciences West room 513, Tucson, AZ 85721, USA  
Tel: 520-621-7982  
Fax: 520-621-1697  
Email: cbm@u.arizona.edu.

TITLE  
JOURNAL

Unpublished (2000)

## COMMENT

Contact: Michalowski, C.B.

FEATURES  
SOURCE

Location/Qualifiers  
1. 575  
/organism="Mesembryanthemum crystallinum"  
/db\_xref="taxon:3544"  
/clone\_lib="MO"  
/tissue\_type="apical meristem and leaf primordia"

/dev\_stage="5 weeks"  
/note="no stress"  
BASE COUNT 150 a 109 c 117 g 199 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1.36e+03 Length: 575  
Score: 41.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 77.78% Mismatches: 0  
Query Match: 93.18% Indels: 0  
DB: 10 Gaps: 0

US-09-698-781-17 (1-9) x BE036163 (1-575)

OY 1 ThrleupheProvalleupheleu 9  
|||||  
DB 157 ACCCTGTTCCGCTCTTTGATCTCTTA 183

RESULT 9  
A2108486

LOCUS A2108486 619 bp DNA linear GSS 09-MAY-2000  
DEFINITION RPCI-23-469G20.TJB RPCI-23 Mus musculus genomic clone  
ACCESSION RPCI-23-469G20, DNA sequence.  
VERSION A2108486  
KEYWORDS A2108486.1 GI:7761463  
GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 619)  
Zhao, S., Niernan, W., Feldblyum, T., Malek, J., Shatsman, S., Akınret,  
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.  
and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-469G20.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
or from Resea.ch Genetics (<http://www.ressea.ch/genetics>) (info@ressea.com). BAC end page:  
[http://www.tigr.org/tcd/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tcd/bac_ends/mouse/bac_end_intro.html)  
Plate: 469 row: 6 column: 20  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
SOURCE

Location/Qualifiers  
1. 619

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-469G20"  
/clone\_lib="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1:  
EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Size  
selected DNA was cloned into the pBACe3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT  
ORIGIN

167 a 150 c 105 g 197 t

Alignment Scores:

Pred. No.:	1.49e+03	Length:	619
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	93.18%	Indels:	0
DB:	17	Gaps:	0

US-09-698-781-17 (1-9) x AZ108486 (1-619)

QY 1 ThirleupheprovalleuLeupheleu 9

DB 452 ACCCTCTTCCCTCTCTCTCTCTC 478

RESULT 10

AU138699/c AU138699 693 bp mRNA linear EST 02-AUG-2002

LOCUS AU138699 PLAC1 Homo sapiens CDNA clone PLAC1009120 5', mRNA

DEFINITION sequence.

ACCESSION AU138699

VERSION AU138699.1 GI:11000220

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.

TITLE HRI human CDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human CDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
Location/Qualifiers  
source 1..693 /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="PLAC1009120"  
/clone\_id="PLAC1"  
/issue\_type="Placenta"  
/note="Vector: pME18SFL3"

BASE COUNT 261 a 124 c 141 g 164 t 3 others

ORIGIN

Alignment Scores:

Pred. No.:	1.72e+03	Length:	693
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	93.18%	Indels:	0
DB:	9	Gaps:	0

US-09-698-781-17 (1-9) x AU138699 (1-693)

QY 1 ThirleupheprovalleuLeupheleu 9

DB 238 ACCTGTTCCCTCTCTCTCTCTG 212

RESULT 11

BG718279/c BG718279 722 bp mRNA linear EST 08-MAY-2001

LOCUS BG718279 NIH\_MGC\_97 Homo sapiens CDNA clone IMAGE:4828598 5',

DEFINITION mRNA sequence.

ACCESSION BG718279

VERSION BG718279.1 GI:13997466

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 722)

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
plate: LLM10746 row: m column: 15  
High quality sequence stop: 718.  
Location/Qualifiers  
source 1..722 /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4828598"  
/clone\_id="NIH\_MGC\_97"  
/lab\_host="DH10B"  
/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcagag); Oligo-dT primed using primer 5'-TTTTTTTTTTT-3', size selected for average insert size 2.2 kb and normalized to ROP 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 261 a 139 c 151 g 171 t

ORIGIN

Alignment Scores:

Pred. No.:	1.81e+03	Length:	722
Score:	41.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	93.18%	Indels:	0
DB:	12	Gaps:	0

US-09-698-781-17 (1-9) x BG718279 (1-722)

QY 1 ThirleupheprovalleuLeupheleu 9

DB 200 ACCTGTTCCCTCTCTCTCTCTG 174

RESULT 12

BE545083/c BE545083 724 bp mRNA linear EST 09-AUG-2000

LOCUS BE545083 60107815F1 NIH\_MGC\_12 Homo sapiens CDNA clone IMAGE:3463851 5',

DEFINITION mRNA sequence.

ACCESSION BE545083

VERSION BE545083

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 724)

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Page 7

```
/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone IMAGE:5415056  
/clone_lib="NH_MGC_87"  
/tissue_type="mammary adenocarcinoma, cell line"
```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-shj-o-03-0-UI"
/clone_1lb="UI-E-EJ0"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="organ: eye; Vector: pRT73-pac (Pharmacia) With a
modified polynuker: Ste1; EOR 1; Ste2; Not 1;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthetasis was primed

```

with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAGAGA; lens, CGATTAGCGA; eye anterior segment, ATGCCGAT; optic nerve, CCATTAGTGG; retina, CCGCG; Retina foveal and Macular, GTCC; RPE and Choroid, ACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 254 a 185 c 227 g 116 t 3 others

## ALIGNMENT SCORES:

Pred. No.: 2.01e+03 Length: 785  
Score: 41.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 88.89% Mismatches: 0  
Query Match: 93.18% Indels: 0  
DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BM715733 (1-785)

OY 1 ThrlaupheProvallLeuleupheleu 9

DB 287 ACCTCTTTCCTCTCTCTCTTTCCTT 261

## RESULT 15

BG574770 813 bp mRNA linear EST 10-APR-2001  
LOCUS 602596822F1 NIH\_MGC\_87 Homo sapiens cDNA clone IMAGE:4705665 5',  
DEFINITION mRNA sequence.

ACCESSION BG574770  
VERSION BG574770.1 GI:13582423

KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 813)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LHAM10572 row: 1 column: 06

High quality sequence stop: 801.

## FEATURES

source

1. 813  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4705685"  
/clone\_1b="NIH\_MGC\_87"  
/tissue\_type="mammary adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: breast; Vector: PCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.383 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## BASE COUNT

247 a 180 c 223 g 163 t

## ALIGNMENT SCORES:

Pred. No.: 2.09e+03 Length: 813  
Score: 41.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 88.89% Mismatches: 0  
Query Match: 93.18% Indels: 0  
DB: 12 Gaps: 0

US-09-698-781-17 (1-9) x BG574770 (1-813)

OY 1 ThrlaupheProvallLeuleupheleu 9

DB 31 ACCTCTTTCCTCTCTCTTTCCTT 5

Search completed: March 14, 2003, 05:26:20  
Job time: 97.2921 secs